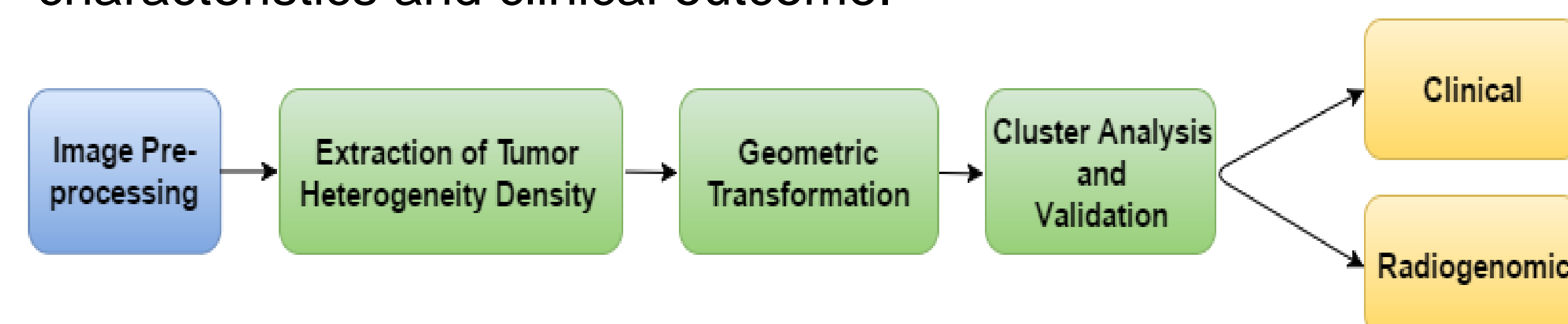


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INTRODUCTION

In this work, we examined MRI images from Glioblastoma Multiforme (GBM) patients to assess image-based tumor heterogeneity. Standard approaches are based on scalar summary measures of histograms (e.g. quantiles) that do not adequately capture the complete information in the voxel-level data. We introduce a novel technique, **DEMARCATE** (Density-based **M**agnetic **R**esonance image **C**lustering for **A**ssessing **T**umor **H**eterogeneity) to explore the entire tumor heterogeneity density profiles. Our analyses revealed two clusters of patients, with marked differences in tumor morphology, genomic characteristics and clinical outcome.



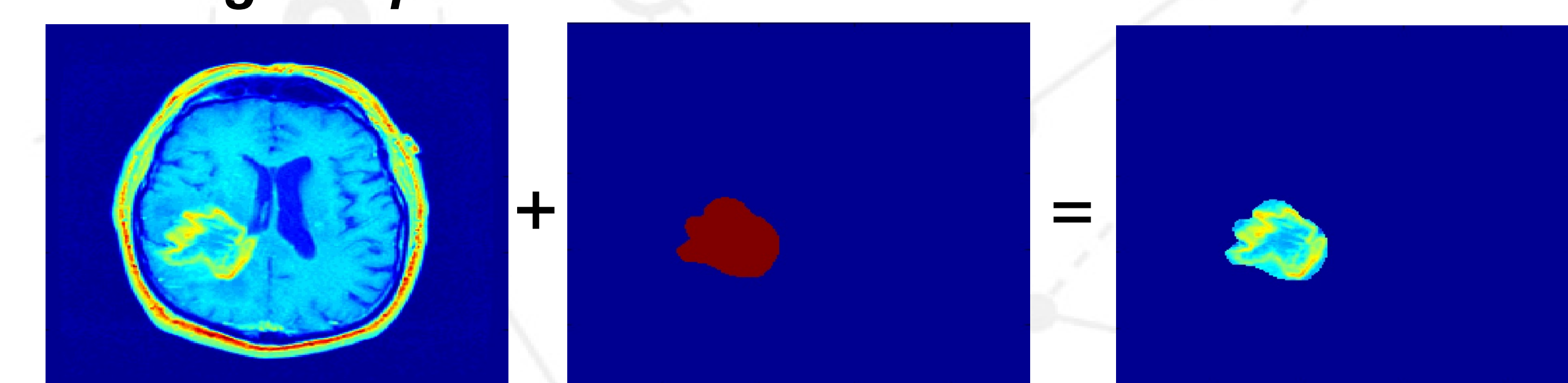
MOTIVATION and AIMS

- Glioblastoma Multiforme (GBM) is the most common and most aggressive malignant primary brain tumor.
- Tumor heterogeneity is a crucial area of cancer research wherein inter- and intra-tumor differences are investigated for assessing and monitoring disease progression.
- Imaging-based modalities allow for non-invasive techniques to assess tumor heterogeneity.

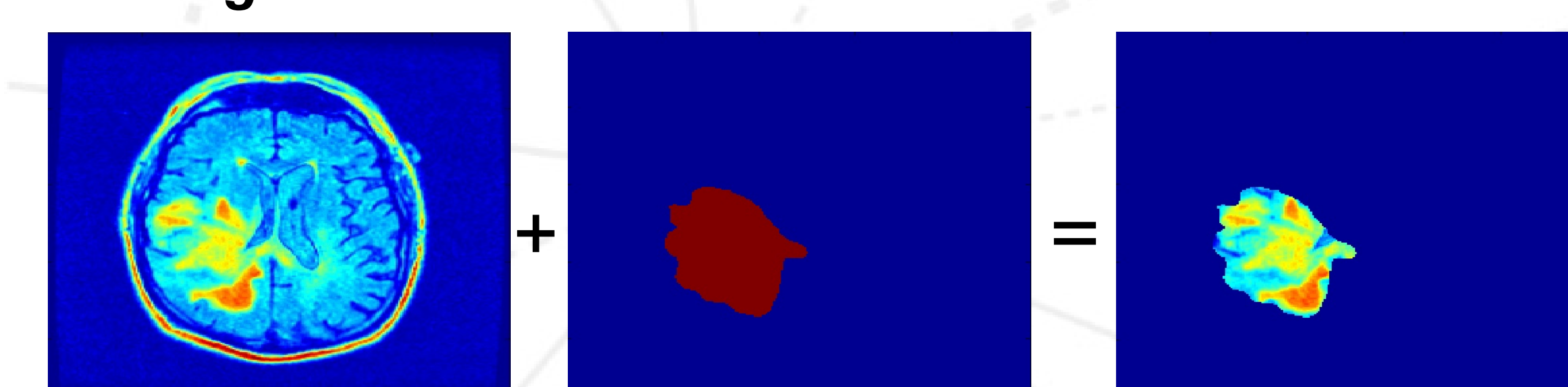
DESCRIPTION OF DATA

Number of patients considered for study: **64**

T1-weighted post contrast



T2-weighted FLAIR

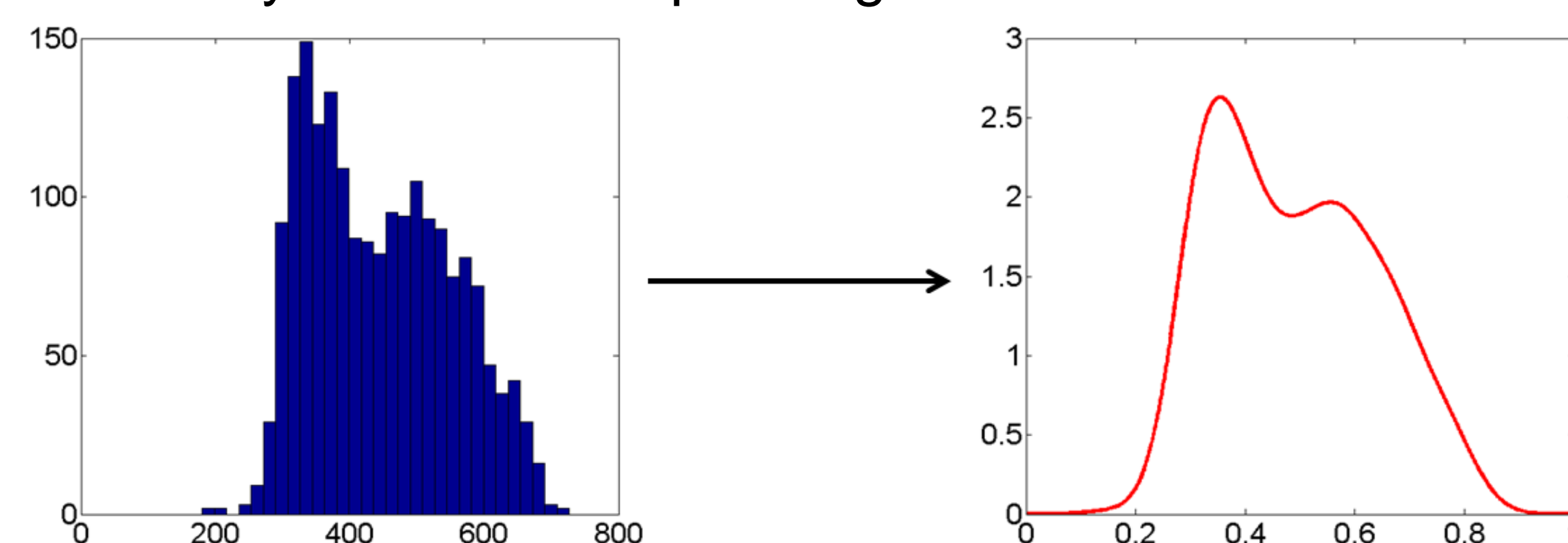


Covariates:
Tumor subtypes – **Classical, Mesenchymal, Neural, Proneural**
Driver genes – **DDIT3, EGFR, KIT, MDM4, PDGFRA, PIK3CA, PTEN**

METHODS

DEMARCATE STATISTICAL FRAMEWORK

Consider a smooth density representation of the histogram for pixel intensity values corresponding to the tumor.



FISHER-RAO METRIC and REPRESENTATION SPACE OF PROBABILITY DENSITY FUNCTIONS

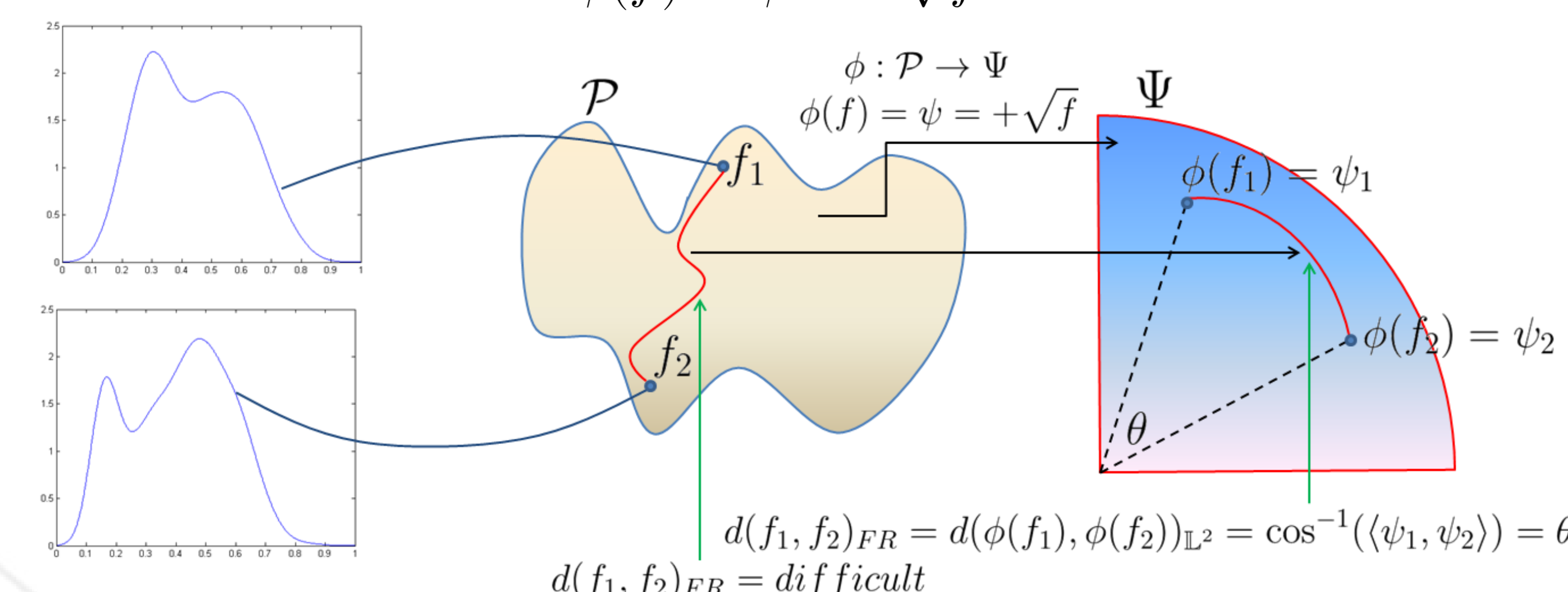
The *Fisher-Rao* (FR) metric on \mathcal{P} is defined as:

for any point $f \in \mathcal{P}$ and the tangent vectors $\delta f_1, \delta f_2 \in T_f(\mathcal{P})$,

$$\langle \delta f_1, \delta f_2 \rangle = \int_0^1 \delta f_1(t) \delta f_2(t) \frac{1}{f(t)} dt$$

Define *square-root transform* of probability density function:

$$\phi(f) = \psi = +\sqrt{f}$$



CLUSTER ANALYSIS and VALIDATION

We utilize an intrinsic version of the *k-means* clustering technique on Ψ . This approach partitions the space by minimizing the within-cluster sum of the squared distances (using the FR metric) to the assigned cluster centre.

For validation, consider a Bayesian version of *Fisher's Test*.

	Cluster 1	Cluster 2	TOTAL	
A	y_1	$n_1 - y_1$	n_1	$y_1 \sim \text{Bin}(n_1, \theta_1)$
A'	y_2	$n_2 - y_2$	n_2	$y_2 \sim \text{Bin}(n_2, \theta_2)$

Let $\theta_1 \sim \text{Unif}(0, 1)$ and $\theta_2 \sim \text{Unif}(0, 1)$ be priors for proportions.

Posterior Distribution: $\theta_i / y_i \sim \text{Beta}(y_i + 1, n_i - y_i + 1)$, $i = 1, 2$.

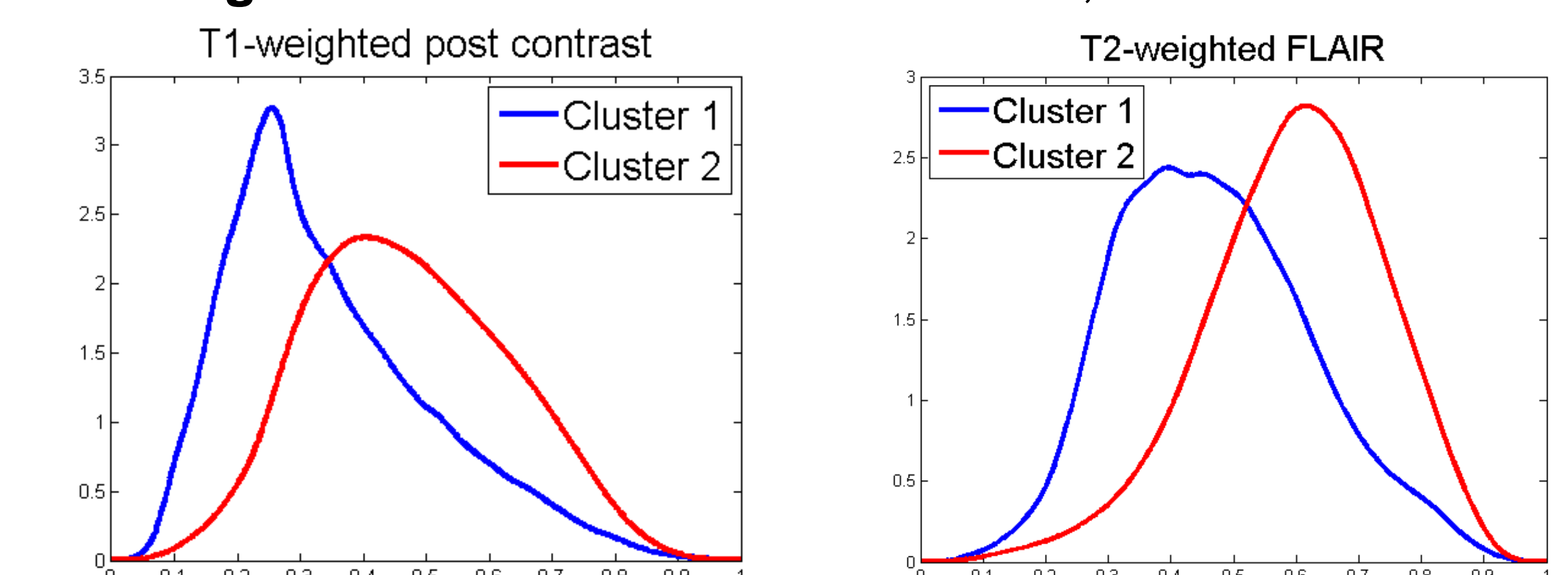
Use Monte Carlo approximation to calculate

Enrichment Probability:

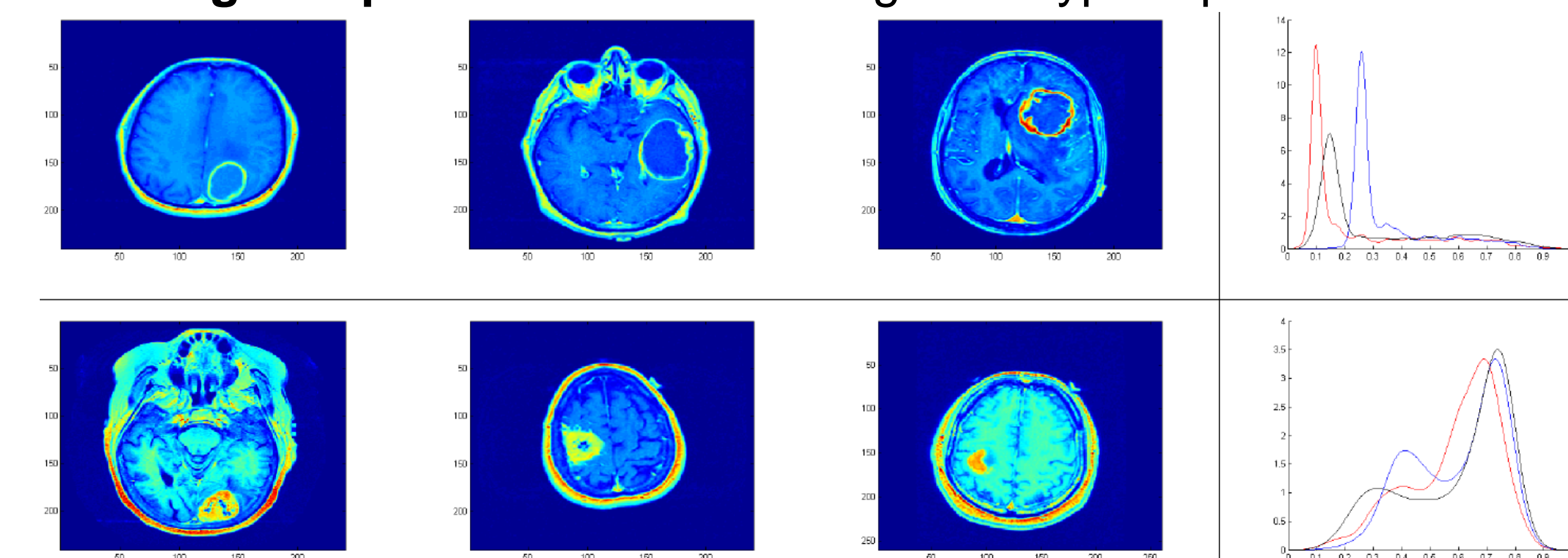
$$\Pr[\theta_1 > \theta_2] \approx \frac{1}{M} \sum_{m=1}^M I(\theta_1^{(m)} > \theta_2^{(m)})$$

RESULTS

T1-weighted post contrast Cluster 1: 24, Cluster 2: 40
T2-weighted FLAIR Cluster 1: 30, Cluster 2: 34



T1-weighted post contrast MR images for typical patients:



T1 MRI			T2 MRI		
1	2		1	2	
		Classical			
		Mesenchymal			
		Neural			
		Proneural			
		DDIT3			
		EGFR			
		KIT			
		MDM4			
		PDGFRA			
		PIK3CA			
		PTEN			

Cluster-wise survival times:

T1-weighted post contrast

	Cl 1	Cl 2	Difference
Mean	22.06	14.81	7.25
Median	17.00	12.95	4.05

T2-weighted FLAIR

	Cl 1	Cl 2	Difference
Mean	20.27	15.11	5.16
Median	16.60	13.45	3.15

CONCLUSION

1 = {high survival} + {Proneural} + {MDM4} + {young patients}
2 = {low survival} + {Classical, Neural} + {KIT, PTEN, DDIT3} + {older patients}

BIBLIOGRAPHY & ACKNOWLEDGEMENTS

Just, N., 2014. *Improving tumour heterogeneity MRI assessment with histograms*. Br. J. Cancer 111 (12), 2205–2213.

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